

RESULT 4

US-08-073-384C-3

; Sequence 3, Application US/08073384C

; Patent No. 5541311

; GENERAL INFORMATION:

; APPLICANT: Dahlberg, James E.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Brow, Mary Ann D.

; TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA

; TITLE OF INVENTION: POLYMERASE

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/073,384C

; FILING DATE: 04-JUN-1993

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/986,330

; FILING DATE: 07-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.

; REGISTRATION NUMBER: 32,837

; REFERENCE/DOCKET NUMBER: FORS-00613

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/705-8410

; TELEFAX: 415/397-8338

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2504 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-073-384C-3

Query Match 1.8%; Score 38.2; DB 1; Length 2504;

Best Local Similarity 47.7%; Pred. No. 0.54;

Matches 112; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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Qy      722 CAGGACCCCCTGCTCATGGGGCTGTTTCCTACTAACCCCAAAGAGAAGACCCAGGAGGAA 781
          | |||      |||| | |      | ||      | | ||      | ||||| || || |
Db      1474 CTGGAAAGGGTGCTCTTTGACGAGCTTAGGCTTCCCGCCTTGGGGAAGACGCAAAGACA 1533

Qy      782 CCCCCTGGCCAGAGCAGGGCCCCCTGTGTTGACCGTGGTGTCCAAGTTCAAGGCCTCACTG 841
          |      ||      | ||| ||| | ||| ||      |      || || | || ||
Db      1534 GGCAAGCGCTCCACCAGCGCCGCGGTGCTGGAGGCCCTACGGGAGGCCACCCCATCGTG 1593
  
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Qy 842 GAGCAGCTTCTGCAGGTCCTACACAGCACCACGCCCCACTACATTCGCTGCATCAAGCCC 901
| | | | | | | | | | | | | | | | | | | | | |
Db 1594 GAGAAGATCCTCCAGCACCGGGAGCTACCAAGCTCAAGAACACCTACGTGGACCCCCTC 1653

Qy 902 AACAGCCAGGGCCAGGCGCAGACCTTTCTCCAAGAGGAGGTCCTGAGCCAGCTGG 956
| | | | | | | | | | | | | | | | | | | | | |
Db 1654 CCAAGCCTCGTCCACCCGAGGACGGGCCGCTCCACACCCGCTTCAACCAGACGG 1708

RESULT 4

US-08-306-691B-46

; Sequence 46, Application US/08306691B

; Patent No. 5734039

; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno

; APPLICANT: Skorski, Tomasz

; TITLE OF INVENTION: ANTISENSE

; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

; STREET: Two Penn Center, Suite 1800

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,691B

; FILING DATE: September 15, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 8321-8

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX: No. 5734039e

; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2638 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-306-691B-46

Alignment Scores:

Pred. No.:	0.0454	Length:	2638
Score:	124.00	Matches:	141
Percent Similarity:	32.45%	Conservative:	55
Best Local Similarity:	23.34%	Mismatches:	227
Query Match:	3.81%	Indels:	181
DB:	1	Gaps:	27

US-09-830-914C-1 (1-612) x US-08-306-691B-46 (1-2638)

Qy 87 HisTyrLeuArgAlaGlnGlnGluGluTyrAlaValGluGlyLeuGluTrpSerPheIle 106

|||:::||||| ||| ||| ::| ::|

Db 559 CATCATCTGCGAGGCCACACAAGGTGCTGGGCAACCGCTGGGCCGAGATCGCCAAGATGTT 618
 Qy 107 AsnTyrGlnAspAsnGlnProCys-----LeuAspLeuIleGluGlySerProIle 123
 :::||| ||| ||| |||:::|
 Db 619 GCCAGGGAGGACAGACAATGCTGTGAAGAATCACTGGAAGCTCTACCATCAAAGGAAGGT 678
 Qy 124 SerIleCysSerLeuIleAsnGluGluCysArgLeuAsnArgProSer----- 139
 |||::: ||||| |||||
 Db 679 GGACACAGGAGGCTTCTTGAGCGAGTCCAAAGACTGCAAGCCCCAGTGTACTTGCTGCT 738
 Qy 140 SerAlaArgGlnLeuGlnThrArgIleGluThrAlaLeuAlaGlySerProCysLeuGly 159
 ||||| ||| ||| |||
 Db 739 GGAGCTCGAGGACAAGGACGGCCTCCAGAGTGCCCGAGCCACGGAAGGCCAGGGAAGTCT 798
 Qy 160 HisAsnLysLeuSerArgGluProSerPheIleValValHisTyrAlaGlyProValArg 179
 :::::|::: |||||::: ||| ||| :::
 Db 799 TCTGACCAACTGGCCCTCCGTCCCTCCTAC-----CATAAAGGAGGAGGAAAACAG 849
 Qy 180 -TyrHis-----ThrAlaGlyLeuValGluLysAsnLysAspProIleProProGluLe 197
 ||| ||| :::::||||| :::|
 Db 850 TGAGGAGGAAGTTCGAGCAGCCACCACATCGAAGGAACAGGAGCCCATCGGTACAGATCT 909
 Qy 197 uThrArgLeuLeuGlnGlnSerGlnAspProLeuLeuMetGlyLeuPheProThrAsnPr 217
 | ::: :::: :::| ||||| ||
 Db 910 GGACGCAGTG-----CGAACACCAGAGCCCTTG-----GAGGAATTCCC 948
 Qy 217 oLysGluLysThrGlnGluGluProProGlyGlnSerArgAlaProValLeuThrValVa 237
 |||| ::: ||||| ||| :::: ||| |||||
 Db 949 GAAGCGTGAGGACCAGGAAGGCTCCCCACCAGAAACGAGCCTGCCTTACAAGTGGGTGGT 1008
 Qy 237 lSerLysPheLys-----AlaSerLeuGluGlnLeuLeuGlnVa 250
 | :::| ||||| ::: ||| ::
 Db 1009 GGAGGCAGCTAACCTCCTCATCCCCGCTGTGGGTCTAGCCTCTCTGAAGCCCTGGACTT 1068
 Qy 250 lLeuHisSerThrThrProHisTyrIleArgCysIleLys----- 263
 :::: ||| ::: |||
 Db 1069 GATCGAGTCGGACCCTGATGCTTGGTGTGACCTGAGTAAATTTGACCTCCCTGAGGAACC 1128
 Qy 264 -----ProAsnSerGlnGlyGlnAlaGlnThrPheLeuGlnGluGl 277
 ||||| ||| ||| |||:::|
 Db 1129 ATCTGCAGAGGACAGTATCAACAACAGCCTAGTGAGCTGCAAGCGTCACATCAGCAGCA 1188
 Qy 277 uValLeuSerGlnLeuGluAlaCysGlyLeuVal----- 288
 :|| |||| ::: |||||
 Db 1189 AGTCCTGCCACCCCGCCAGCCTTCCGCCCTGGTGCCAGTGTGACCGAGTACCGCCTGGA 1248
 Qy 289 -----GluThrIleHisIleSerAl 295
 ||| ||| |||||
 Db 1249 TGGCCACACCATCTCAGACCTGAGCCGGAGCAGCCGGGGCGAGCTGATCCCCATCTCCCC 1308
 Qy 295 aAla-----GlyPheProIleArgValSerHisArgAsnPh 307
 ::: ||| ||| ||| |||
 Db 1309 CAGCACTGAAGTCGGGGGCTCTGGCATTGGCACACCGCCCTCTGTGCTCAAGCGGCAGAG 1368
 Qy 307 eValGluArgTyrLysLeu-----LeuArgArgLeuHi 318
 ||| ||| ||| |||
 Db 1369 GAAGAGGCGTGTGGCTCTGTCCCTGTCACTGAGAATAGCACCAGTCTGTCTTCTTCCGGA 1428

Qy 318 sProCysThrSerSerGlyProAspSerProTyrProAlaLysGlyLeuPro----- 335
 ||| ||| ||| ||| ||| ||| ||| |||
 Db 1429 TTCCTGTAACAGCCTCACGCCCAAGAGCACA---CCTGTTAAGACCCTGCCCTTCTCGCC 1485
 Qy 336 -----GluTrpCysProHisSerGluGluAlaThrLeuGluProLeuIl 350
 ||| ::::: ||||| |||
 Db 1486 CTCCCAGTTTCTGAACTTCTGG-----AACAAACAGGACACATTGGAG---CTGGA 1533
 Qy 350 eGlnAspIleLeuHisThrLeuProValLeuThrGlnAlaAlaAlaIleThrGlyAspSe 370
 ||| :: ||||| ::||| ::|||
 Db 1534 GAGCCCCTCGCTGACATCCACCCAGTGTGCAGCCAGAAGGTGGTGGTCACC----- 1585
 Qy 370 rAlaGluAlaMetProAlaProMetHisCysGlyArgThrLysValPheMet-ThrAspS 390
 |||::||| ||| ||| ::||| :
 Db 1586 -----ACACCACTGCAC-----CGGGACAAGACACCCCTGCACCAGAA 1623
 Qy 390 erMetLeuGluLeu----- 394
 ::||| |||
 Db 1624 ACATGCTGCGTTTGTAAACCCAGATCAGAAGTACTCCATGGACAACACTCCCCACACGCC 1683
 Qy 395 -----LeuGluCysGlyArgAlaA 401
 ||| ||| |
 Db 1684 AACCCCGTTCAAGAACGCCCTGGAGAAGTACGGACCCCTGAAGCCCCTGCCACAGACCCC 1743
 Qy 401 rgValLeuGluGlnCys---AlaArgCysIleGln-GlyGlyTrpArgArg-----His 417
 || :: ||||| ||||| ||| |||
 Db 1744 GCACCTGGAGGAGGACTTGAAGGAGGTGCTGCGTTCTGAGGCTGGCATCGAACTCATCAT 1803
 Qy 418 ArgHisArgGluGlnGluArgGlnTrpArgAlaValMetLeuIleGlnAlaAlaIleArg 437
 ||| ||| ||| ||| ::|||
 Db 1804 CGAGGACGACATCAGGCCCGA-----GAAGCAGAAGAGGAA 1839
 Qy 438 SerTrp-LeuThrArgLysHisIleGlnArgLeuHisAlaAlaAlaThrValIleLysAr 457
 ::||| ||| ||| |||::: ::
 Db 1840 GCCTGGGCTGCGGCGAGCCCCATCAAGAAAGTCCGGAAGTCT----- 1882
 Qy 457 gAlaTrpGlnLysTrpArgIleArgMetAlaCysLeuAlaAlaLysGluLeuAspGlyVa 477
 ||||| ::|||
 Db 1883 -----CTGGCTCTTGACATTGTGGATGAGGA 1908
 Qy 477 lGluGluLysHisPheSerGlnAlaProCysSerLeuSer-----ThrSerProLe 494
 :: ||| ||| ||||| |||::: |||
 Db 1909 TGTGAAGCTGATGATGTCCACACTGCCCAAGTCTCTATCCTTGCCGACAACAGCCCTTC 1968
 Qy 494 uGlnThrArgLeuLeuGluAlaIleIleArgLeuTrpProLeuGlyLeuValLeuAlaAs 514
 :: ||| |||:: |||
 Db 1969 AAACCTCTCCAGCCTCACCCCTG-----TCAGGTATCAAAGAAGACAA 2010
 Qy 514 nThrAlaMetGlyValGlySerPheGlnArgLysLeuValValTrpAlaCysLeuGlnLe 534
 |::: :: ||| ||| ||| ||| |||
 Db 2011 CAGCTTGCTCAACCAGGGCTTCTTGCAGGCCAAGCCCGAGAAGGCAGCAGTGGCCAGAA 2070
 Qy 534 uProArgGlySerProSerSerTyrThrValGlnThrAlaGlnAspGlnAla-GlyValT 554
 ||||| ||| ::||| ||| |||
 Db 2071 GCCCCGA-----AGCCACTTCACGACACCTGCCCTATGTCCAGTGCCTGGA---- 2117

Qy 554 hrSerIleArgAlaLeuProGlnGly-----SerIleLysPheHisCysArgLysSerP 572
||| ||| ||| ||| |||::: |
Db 2118 -----AGACGGTGGCCTGCGGGGGGACCAGGGACCAGCTTTTCATGCAGGAGAAAGC 2169

Qy 572 ro 572
||
Db 2170 CC 2171